

## **AMENDMENTS TO THE SPECIFICATION:**

Please amend the paragraphs on page 5, lines 21-34 as follows:

Fig. 1 provides a schematic structure of the RP-II protease from *Bacillus licheniformis*, BLC (SEQ ID NO: 2).

Fig. 2 shows a 3D structure based alignment of the wild type RP-II proteases 1 to 8 of Table 1 (SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14 and 16).

Please amend the paragraphs on page 15, lines 5-10 as follows:

The overall structure of BLC falls into the S1 group of the proteases (MEROPS; <http://merops.sanger.ac.uk/>). The structure is a trypsin type of fold with two beta-barrel domains. The beta-barrel's each consists of six antiparallel beta-sheets folded into a beta-barrel. The topology can be described as S1-S2-S3-S6-S5-S4 for the strands in both beta-barrels. It is assumed that all the RP-II proteases fall within the same general overall structure.